

## SEQUENCE LISTING



## (1) GENERAL INFORMATION:

- (i) APPLICANT: TAKESHI NAKAMURA
- (ii) TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: PILLSBURY, MADISON & SUTRO
  - (B) STREET: 1100 NEW YORK AVENUE, N.W.
  - (C) CITY: WASHINGTON
  - (D) STATE: D.C.
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: FLOPPY DISK
  - (B) COMPUTER: IBM PC COMPATIBLE
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: U.S. 09/054,492
  - (B) FILING DATE: APRIL 3, 1998
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: PAUL E. WHITE, JR.
  - (B) REGISTRATION NUMBER: 32,011
  - (C) REFERENCE/DOCKET NUMBER: 7898/252159
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (202) 861-3000
  - (B) TELEFAX: (202) 822-0944
  - (C) TELEX: 6714627CUSH

## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Lys Phe Pro Gly Pro Leu Glu Asn Gln Arg Leu Ser Phe Leu  
5 10 15

Leu Glu Lys Ala Ile Thr Arg Glu Ala Gln Met Trp Lys Val Asn  
20 25 30

Val	Arg	Lys	Met	Pro	Ser	Asn	Gln	Asn	Val	Ser	Pro	Ser	Gln	Arg
			35						40				45	
Asp	Glu	Val	Ile	Gln	Trp	Leu	Ala	Lys	Leu	Lys	Tyr	Gln	Phe	Asn
			50			55				60				
Leu	Tyr	Pro	Glu	Thr	Phe	Ala	Leu	Ala	Ser	Ser	Leu	Leu	Asp	Arg
			65				70				75			
Phe	Leu	Ala	Thr	Val	Lys	Ala	His	Pro	Lys	Tyr	Leu	Ser	Cys	Ile
			80				85				90			
Ala	Ile	Ser	Cys	Phe	Phe	Leu	Ala	Ala	Lys	Thr	Val	Glu	Glu	Asp
			95					100				105		
Glu	Arg	Ile	Pro	Val	Leu	Lys	Val	Leu	Ala	Arg	Asp	Ser	Phe	Cys
			110				115				120			
Gly	Cys	Ser	Ser	Ser	Glu	Ile	Leu	Arg	Met	Glu	Arg	Ile	Ile	Leu
			125				130				135			
Asp	Lys	Leu	Asn	Trp	Asp	Leu	His	Thr	Ala	Thr	Pro	Leu	Asp	Phe
			140				145				150			
Leu	His	Ile	Phe	His	Ala	Ile	Ala	Val	Ser	Thr	Arg	Pro	Gln	Leu
			155				160				165			
Leu	Phe	Ser	Leu	Pro	Lys	Leu	Ser	Pro	Ser	Gln	His	Leu	Ala	Val
			170				175				180			
Leu	Thr	Lys	Gln	Leu	Leu	His	Cys	Met	Ala	Cys	Asn	Gln	Leu	Leu
			185				190				195			
Gln	Phe	Arg	Gly	Ser	Met	Leu	Ala	Leu	Ala	Met	Val	Ser	Leu	Glu
			200				205				210			
Met	Glu	Lys	Leu	Ile	Pro	Asp	Trp	Leu	Ser	Leu	Thr	Ile	Glu	Leu
			215				220				225			
Leu	Gln	Lys	Ala	Gln	Met	Asp	Ser	Ser	Gln	Leu	Ile	His	Cys	Arg
			230				235				240			
Glu	Leu	Val	Ala	His	His	Leu	Ser	Thr	Leu	Gln	Ser	Ser	Leu	Pro
			245				250				255			
Leu	Asn	Ser	Val	Tyr	Val	Tyr	Arg	Pro	Leu	Lys	His	Thr	Leu	Val
			260				265				270			
Thr	Cys	Asp	Lys	Gly	Val	Phe	Arg	Leu	His	Pro	Ser	Ser	Val	Pro
			275				280				285			
Gly	Pro	Asp	Phe	Ser	Lys	Asp	Asn	Ser	Lys	Pro	Glu	Val	Pro	Val
			290				295				300			
Arg	Gly	Thr	Ala	Ala	Phe	Tyr	His	His	Leu	Pro	Ala	Ala	Ser	Gly
			305				310				315			

Cys Lys Gln Thr Ser Thr Lys Arg Lys Val Glu Glu Met Glu Val  
 320 325 330  
 Asp Asp Phe Tyr Asp Gly Ile Lys Arg Leu Tyr Asn Glu Asp Asn  
 335 340 345  
 Val Ser Glu Asn Val Gly Ser Val Cys Gly Thr Asp Leu Ser Arg  
 350 355 360  
 Gln Glu Gly His Ala Ser Pro Cys Pro Pro Leu Gln Pro Val Ser  
 365 370 375  
 Val Met

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG AAG TTT CCA GGG CCT TTG GAA AAC CAG AGA TTG TCT TTC CTG	45
TTG GAA AAG GCA ATC ACT AGG GAA GCA CAG ATG TGG AAA GTG AAT	90
GTG CGG AAA ATG CCT TCA AAT CAG AAT GTT TCT CCA TCC CAG AGA	135
GAT GAA GTA ATT CAA TGG CTG GCC AAA CTC AAG TAC CAA TTC AAC	180
CTT TAC CCA GAA ACA TTT GCT CTG GCT AGC AGT CTT TTG GAT AGG	225
TTT TTA GCT ACC GTA AAG GCT CAT CCA AAA TAC TTG AGT TGT ATT	270
GCA ATC AGC TGT TTT TTC CTA GCT GCC AAG ACT GTT GAG GAA GAT	315
GAG AGA ATT CCA GTA CTA AAG GTA TTG GCA AGA GAC AGT TTC TGT	360
GGA TGT TCC TCA TCT GAA ATT TTG AGA ATG GAG AGA ATT ATT CTG	405
GAT AAG TTG AAT TGG GAT CTT CAC ACA GCC ACA CCA TTG GAT TTT	450
CTT CAT ATT TTC CAT GCC ATT GCA GTG TCA ACT AGG CCT CAG TTA	495
CTT TTC AGT TTG CCC AAA TTG AGC CCA TCT CAA CAT TTG GCA GTC	540
CTT ACC AAG CAA CTA CTT CAC TGT ATG GCC TGC AAC CAA CTT CTG	585
CAA TTC AGA GGA TCC ATG CTT GCT CTG GCC ATG GTT AGT CTG GAA	630
ATG GAG AAA CTC ATT CCT GAT TGG CTT TCT CTT ACA ATT GAA CTG	675

CTT CAG AAA GCA CAG ATG GAT AGC TCC CAG TTG ATC CAT TGT CGG 720  
GAG CTT GTG GCA CAT CAC CTT TCT ACT CTG CAG TCT TCC CTG CCT 765  
CTG AAT TCC GTT TAT GTC TAC CGT CCC CTC AAG CAC ACC CTG GTG 810  
ACC TGT GAC AAA GGA GTG TTC AGA TTA CAT CCC TCC TCT GTC CCA 855  
GGC CCA GAC TTC TCC AAG GAC AAC AAG CCA GAA GTG CCA GTC 900  
AGA GGT ACA GCA GCC TTT TAC CAT CAT CTC CCA GCT GCC AGT GGG 945  
TGC AAG CAG ACC TCT ACT AAA CGC AAA GTA GAG GAA ATG GAA GTG 990  
GAT GAC TTC TAT GAT GGA ATC AAA CGG CTC TAT AAT GAA GAT AAT 1035  
GTC TCA GAA AAT GTG GGT TCT GTG TGT GGC ACT GAT TTA TCA AGA 1080  
CAA GAG GGA CAT GCT TCC CCT TGT CCA CCT TTG CAG CCT GTT TCT 1125  
GTC ATG TA  
1133

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CGTTCCCGGG TATGAAGTTT CCAGGGCCTT TGG

33

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACGGCTCGAG CTACATGACA GAAACAGGCT G

31

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Glu Asp Asn Val Ser Glu Asn Val Gly Ser Val Cys Gly Thr  
5   10